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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 05:10:54 ; Search time 1866 Seconds

(without alignments)
9842.273 Million cell updates/sec

Title: US-10-091-628-1

Perfect score: 1134
Sequence: 1 atgagagcattgttccag.....acatcattcatggaatag 1134

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

ched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
5: em_estba:*
6: em_estba:*
7: em_estba:*
8: em_estba:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_fod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	704.4	62.1	2125	11	AK018423	Mus muscu
2	450.4	39.7	652	10	BB613812	BB613812
3	335.4	29.6	972	12	BB613812	BB613812
4	327.4	28.9	356	10	BB618126	BB618126
5	200	17.6	658	10	BB625035	BB625035
6	200	17.6	662	10	BB664585	BB664585

7	194.2	17.1	642	9	AU176916	AU176916
8	189	16.7	760	13	BT668670	BT668670
9	184	16.2	274	10	BE151388	BE151388
10	182.6	16.1	543	17	AQ013853	AQ013853
11	164.6	14.5	538	10	BE030429	BE030429
12	162.4	14.3	686	10	AM107022	AM107022
13	149.4	13.2	666	10	BB625042	BB625042
14	142.2	12.5	919	13	BI149148	BI149148
15	141.2	12.5	876	13	BE234728	BE234728
16	140.4	12.4	307	10	BB605283	BB605283
17	140.4	12.4	419	10	BB846568	BB846568
18	138	12.2	628	10	BE031975	BE031975
19	137.6	12.1	803	9	AI528386	AI528386
20	137.4	12.1	928	12	BE236073	BE236073
21	136.8	12.0	632	13	BI218113	BI218113
22	136.4	12.0	404	10	AW786072	AW786072
23	136.4	11.7	846	13	BI144614	BI144614
24	131.4	11.6	799	13	BI331108	BI331108
25	130	11.5	476	9	AI303923	AI303923
26	128	11.3	410	9	AI046372	AI046372
27	127.2	11.2	860	13	BI339089	BI339089
28	123.8	10.9	511	13	BI180877	BI180877
29	121.4	10.7	668	10	BE439690	BE439690
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31	107.6	9.5	615	14	BM755816	BM755816
32	105.8	9.3	465	17	AZ457444	AZ457444
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34	103.4	9.1	974	12	BF235598	BF235598
35	103.2	9.1	1091	17	CNS0380W	CNS0380W
36	101.6	9.0	853	12	BF312464	BF312464
37	101.4	8.9	633	10	BE439637	BE439637
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41	92	8.1	831	9	AL530028	AL530028
42	90.2	8.0	464	12	BF043423	BF043423
43	89.6	7.9	602	9	AI119397	AI119397
44	87	7.7	525	10	BB668323	BB668323
45	85.4	7.5	378	9	AI386052	AI386052

ALIGNMENTS

RESULT 1
LOCUS AK018423
DEFINITION Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430417G17; similar to ILEAL NA+-DEPENDENT BILE ACID TRANSPORTER (ISBT), full insert sequence.
ACCESSION AK018423
VERSION AK018423.1 GI:12858114
KEYWORDS HTc; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 16 days embryo lung cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library
clone:8430417G17.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
PUBMED 99279253
JOURNAL MEDLINE
PUBMED 10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE
PUBMED 20499374
PUBMED 11042159


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QY 541 TATGTAATTACAGATGGCCAAACATCCAAATCATCTCAAGATTGGGCGCTTGT 600
DB 713 TATGTAATTACAGATGGCCAAACATCCAAATCATCTCAAGATTGGGCGCTTGT 772
QY 601 GGTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
DB 773 GGTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 829
QY 661 AATTGACATCAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 830 AACACAGACATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 889
QY 721 GCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
DB 890 GCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 949
QY 781 GAACTGAGAGCTCAGAAATTTAGATGTCATCACCATGCTCCAGTTATCTTCACT 840
DB 950 GAACTGAGAGCTCAGAAATTTAGATGTCATCACCATGCTCCAGTTATCTTCACT 1009
QY 841 GAGCACTGTCAGATGTTGATGTTCCACTGCTTATGACTCTTCCAGCTGATAGT 900
DB 1010 GAGTACTGTCAGATGTTGATGTTCCACTGCTTATGACTCTTCCAGCTGCTG 1069
QY 901 GATTTCTTATGTTGACATATATGACATGATGACAGAGAGATGGAACAATGGA 960
DB 1070 GGGCTGCTATCTGTCGACATATGACATGATGACAGAGAGATGGAACAATGGA 1129
QY 961 AAAAAGAACTAGGTTGACAGAGATGTCGATGAGAGAAATGCACTTCTTCCAGAG 1020
DB 1130 AGACAGACATCCGATGATGTCGACATGCTCTCTCTCTCTCTCTCTCTCTCT 1180
QY 1021 ACCATGCTTCTTCTGAGTGAATGAAGAAGTGCATCTCTGCGGACACAGGCGCA 1080
DB 1181 ACCATGCTTCTTCTGAGTGAATGAAGAAGTGCATCTCTGCGGACACAGGCGCA 1240
QY 1081 ATGATGTCAGAGGCTCTGAGGCGGATGAGGCGGATGAGGCGGATGAGGCGG 1134
DB 1241 GAGCAGCAGCAGAGGCTCTGAGGCGGATGAGGCGGATGAGGCGGATGAGGCGG 1294

RESULT 2
LOCUS BB613812 652 bp mRNA linear EST 26-OCT-2001
DEFINITION BB613812 RIKEN full-length enriched, 0 day neonate head Mus
VERSION BB613812
KEYWORDS BB613812.1 GI:16454310
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Harz,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koude,
M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muraetsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
TITLE Laboratory for Genome Exploration Research Group, RIKEN Genomic
JOURNAL Sciences Center (GSC), Yokohama Institute
COMMENT The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/

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FEATURES

source

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muraetsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

Wagii, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muraetsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational analysis of full-length mouse cDNAs compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

location/Qualifiers

source

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1. 652
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4831431E11"
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head"

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/sex="mixed"
/tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGAGAGAGAGATCCAGAGGCTTTTCTTTTCTTTTCTTTT 3'. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence 15' GAGAGAGAGATCCAGAGTGAATTAATTAATCCCCCCCCC
3'. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda PLC I."

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BASE COUNT

ORIGIN

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118 a 172 c 173 g 189 c
Query Match 39.7%; Score 450.4; DB 10; Length 652;
Best Local Similarity 81.7%; Pred. No. 2.8e-119;
Matches 533; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

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QY 92 AGCTGTTTACAGATGTCACCTGAGAGAGGCGGCTGTCATGTTCTTTGGAT 151
DB 4 AGCTGTTTACAGATGTCACCTGAGAGAGGCGGCTGTCATGTTCTTTGGAT 63
QY 152 GTTCGAGAGATCGAAGCTGTGTGCAATCAGAGAGCCCTGGGCAATGTGTGG 211
DB 64 GTTCGAGAGATCGAAGCTGTGTGCAATCAGAGAGCCCTGGGCAATGTGTGG 123
QY 212 GACTGCTGTCAGATGTCATGCTTTTACAGCTTATCTCTGCGCAATGACTTT 271
DB 124 GCTGCTTCCAGATGTCATGCTTGAAGAGCTTATCTGTAGCCATGTGCTTGG 183

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Oy	272	CTCTAAGCAAGTCCAAAGCTATTTGGCTGTCTCATATATGGGCTGTGCCCGGGGGGACCA	331
Dd	184	GTCTAAACCATTCCAAGCTATTGCTGTCTCTATATATGGGAGCTGTCCCTGGGGGACCA	243
Oy	332	TCTCTAACATTTTCACCTTCTGGGTATGATGAGATATGGATCTCAGCATCAGTATGACA	391
Dd	244	TCTCTAAAGTTTCTCACCTTCTGGGTATGAGAGATATGATCTCAGCATCAGTATGACA	303
Oy	392	CCGTGTCACCGTGGCCGCGCTGGGAAATGATGCACTCGCATTTATCTTACACCTGGT	451
Dd	304	CTGTGTTCCAGATGGCCGCGCTGGGAAATATCTCTCTGCTCTACATCTACACCGGT	363
Oy	452	CCTGAGTCTTTCAGCAGAACTCACCATTCCTTATCAGAACATAGGAATTACCTTGTGT	511
Dd	364	CCTGAGCTCTGACAGAACTCTGTCACTCCGTATCAGAGCATAGGAATTTACCTTGTGT	423
Oy	512	GCTTACCATTTCTCTGTGGCTTGTGTGTATGTAAATTAACAGATGGCCAAACATCA	571
Dd	424	CCCTGTGGTTCTCTGTGGCTTGTGGCGTATGTAAATTAATAGTGGCCAAAGCAGACA	483
Oy	572	AAATGATTTCTCAAGATTTGGGGCCGTTGTGTGTGGGGTCTCTCTCTGTGGTGTGGAGTTG	631
Dd	484	CGGTATTTCTCAAGTCCGAGCCATTTCTGGGTGCGATGTCCTCTCTGTGTGTGGCAGTTA	543
Oy	632	CTGTGTGTGCTCTGGCGAAAGGATCTTGAATTCAGACATCAACCTTCTGACCATCAGTT	691
Dd	544	CTGGCATGTCTCTGGCAAAAGG---CTGGAAACACAGACGTCACTTCTGTGTATCAGCT	600
Oy	692	TCATCTTTCCTTGAATTTGGCCATGTCAAGGGTTTTCTGTGGACATTTTTAC	743
Dd	601	GCATTTTCCCTTGGTCGGCATTGACAGGCTCTCTGTGGGCAATTTCTAC	652

RESULT 3					
BG872314	BG872314	972 bp	mRNA	linear	EST 29-MAY-2001
LOCUS	60279097771	NCI	CGAP	SGS	Mus musculus cDNA clone IMAGE:4922227 5',
DEFINITION	mRNA sequence.				

ACCESSION	EG872314	GI:14222854
VERSION	EG872314.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE 1 (bases 1 to 972)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL0841 row: j column: 20
High quality sequence set: 786.

FEATURES	SOURCE
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NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
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Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      222 a      277 c      263 g      210 t

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ORIGIN

Query Match	29.6%;	Score 335.4;	DB 12;	Length 972;
Best Local Similarity	-73.8%;	Pred. No. 6.9e-86;		
Matches 458;	Conservative 0;	Mismatches 151;	Indels 12;	Gaps 2;

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OY	574	ATCATCTTCAGAAATTTGGGGCCGTGTGGTGGTGGGGTCTCTCTTCTGTGGTGCAGTGGCT	633
Db	61	GTATTTCTCAAGGTGGAGGCATCTGTGGTGGCATGTGCTCTGTGGTGGTGGCATTTACT	120
OY	634	GGTGTGGTCTCTGGCGAAAGAGATCTTGGAAATTCAGACATCACTTCTTGCATCATAGTTTC	693
Db	121	GGCATGTGCTCTGGCAAAAG---CTGAAACACAGACGTCACTCTTCTGGTATCAGCTGC	177
OY	694	ATCTTTCCTTTGATTGGCAATGTGACGGGTTTTTGTGTCGACATTTTAAACCAACAGTCT	753
Db	178	ATTTTCCCTTTGGTGTGGCCATGTACAGGCTTCTGTGGATTCCTCACCCACCAATCT	237
OY	754	TGGCAAGGTGCAGAGACAATTTCTTGAACAACTGAGCTCAGAAATTTAGATGTGCATC	813
Db	238	TGGCAAGGTGCAGAGACCATTTCTCATAGAGACTGGCGCTCAGAACATTCACCTGTGCATC	297
OY	814	ACCATGCTCCAGTTATCTTTCACTGCTGAGAGACTTTGGTCCAGATTTGAATTTCCACTG	873
Db	298	GCCATGTGCAGCTGCTCTTCTGTGTGAGTAAGTCTGGTCCAGCTGTAACTTTGCATGG	357
OY	874	GCCATGTGACTCTTCCAGCTGATGATGAGATTTCTTATTTGTGAGCATATCAGACGTAC	933
Db	358	GCCATGTGACTCTTCCAGGTGCTGCAAGGCGTGTCTATGTGTGACAGATATCAGGACATAC	417
OY	934	AAGAGAGATTTGAAGAACAAATCAGAAAAAAGAACTCAGTTGCAAGAAGTCTGCAAT	993
Db	418	AAGAGAGAGCGAAGAGATTAATGCAGAGACAGACCCGAGATTCACAGAGTCTGCTAC	477
OY	994	ACGAGAGAAATGACTTCTTCCAGAGAGCCCAATGCTCTTGAAGGTGAATGAAGAAAGT	1053
Db	478	GAGAAAGCA-----GCCAGAGAGACCAAGTCTTTCTTGGATTAAGGGGATGAGGCT	528
OY	1054	GCCATCACTCTGGGCGAACAGGGCCAAATGATTTGCCACAGGGCTCTTGAGCCAGTTGGC	1113
Db	529	GCCTTAATCTGTGGGCGCAGTGCACACCGAGAGACACAGGGCTGTGAAGTGAATGAC	588
OY	1114	CACATCACTTATGTGAATAG 1134	
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RESULT 4	BE181226	356 bp	mRNA	linear	EST 22-JUN-2000
LOCUS	BE181226				
DEFINITION	BE181226	CMW-H10630-220300-125-F05	H10630	Homo sapiens cDNA,	mRNA sequence.
ACCESSION	BE181226				
VERSION	BE181226.1	GI:8660402			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
1 (bases 1 to 356)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE	JOURNAL	YEAR	PAGE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7)	3491-3496 (2000)
20202663			

QY	241	TTTAAAGCTTATCTCTGCGCATTAAGCTTTTCTCTGAAGCCAGGTCACGATTAAGCTT	300
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QY	301	CTCATCATGAGGCTGCTGCGCCGGGGGACACATCTCTAAACATTTACCTTGGGTTGAT	360
DB	319	CAATATGATGGGAGCGCTGCGCTGGGGGACACATGTTGAAGGTCGTAACCTTGGGGTTGA	378
QY	361	GGAGTATGATCTCA	376
DB	379	GGAGTATGATCTCA	394
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ACCESSION	AU176916		linear
VERSION	AU176916.1	GI:13425752	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
BASE COUNT			
Query Match			
Best Local Similarity			
Matches			
QY	109	GTGTCCACTGTGATGATGAGGAGCTGCTCATGTTCTTTGGATGTTCCGTGGAGATCCGG	168
DB	228	GTGTCTACATGTCATGCTGCGCCATGATGATGTTCCGATGGCTGACCGGTGACTTCTGG	287
QY	169	AAGCTGTGTGGCAATCAGAGAGACCTTGGGGCATTTGCTGTGGAGCTGCTTCCAGTTT	228
DB	288	AAGCTGTGGGATCAATCAGAGACCTTGGGGCATGTCATGCGCTTCAATCTGCCAGTTT	347
QY	229	GGGCTATAGCCCTTTTACAGACTTATCTCTGGGCAATTAAGCTTTTCTCTGAAGCCAGTCAA	288
DB	348	GGCATCATGTCCTTACAGGCTTGGCGCTTGGCTCTTCAAGCTTCTGCTGTGACG	407
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Db	468	TACTGGCTGATVAGAGACATGAGACTGAGCTGACATGATATGACGAGCTGTTCCTCATCTCG	527	
Oy	409	GCCCTGGGAATGATAGCCACTGTGCATTTATCTTACAACCTGTCTCTGAGTCTTCAGAG	468	
Db	528	GCCCTGGGAGATAGGCCCTTGTCTGTTCATCTACAACAGCGTGTGAGACCTTCAGAGCAC	587	
Oy	469	AATCCACCATTTCTCTTATCAGAATAATGATATCCCTTGTGTGCTCAGCATTC	523	
Db	588	TCTATCATGATCCCCCTTTGACAGCATCGGATCAGCGTGGCGGCTTCTGATTC	642	
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	LOCUS			
	DEFINITION	B1768670	760 bp	mRNA linear EST-25-SEP-2001
	ACCESSION	6030572221	NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5206781 5'	
	VERSION	B1768670		
	KEYWORDS	B1768670.1 GI:15760248		
	SOURCE	EST.		
	ORGANISM	human.		
	REFERENCE	Homo sapiens		
	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	JOURNAL	1 (bases 1 to 760)		
	COMMENT	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LHAM1518 row: k column: 06 High quality sequence stop: 760.		
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	source	Location/Qualifiers		
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		/lab_host="DH10B"		
		/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6, Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed, and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note this is a NIH_MGC library."		
	BASE COUNT	181 a 185 c 190 g 204 t		
	ORIGIN			
	Query Match	16.7%; Score 189; DB 13; Length 760;		
	Best Local Similarity	62.9%; Pred. No. 1.7e-43;		
	Matches	325; Conservative 0; Mismatches 190; Indels 2; Gaps 2		
Oy	80	ATGAAACCTGAGAGCTCGTTTACACAGTGTCCATCTGATGATGAGGAGCTGCTCATGT	139	
Db	245	ATAACATCTTAAGTGTGTTCTTAGTAGCGGAGTCAGAACCATCCTGTGTGAGCTTGATGT	304	
Oy	140	TCTCTTTGGATGTTCCTGTGAGATCCGGAAGCTGTGTGCCACATCAGAGAGACCTTGGG	199	

Db 305 TCTCCATGGAGCAAGTGGAAATTCATAGAAATTTCTAGGGCAATTAAGCCGCGCTGGG 364
Oy 200 GGATTCGCTGGAGACTGCTCTGCGAGTTGGGCTCAATGCTTTACAGCTTATCTCTGG 259
Db 365 GCATTTGTGTGGCTTCTCTGTCATTTGGATCATTGCCCCACAGAGATTATCTCTGT 424
Oy 260 CCATTAGCTTTTCTCTGAAAGCCAGTCCAAAGCTTATGCTGTTCTCATCATGAGGCTGCTGCC 319
Db 425 CGGTGGCTTTTGAACATCTCCCGCTCAGGCGCTAGTGGTGCCTATTAAGATGCTGCGC 484
Oy 320 CGGGGGGGCAACATCTCTAATTTTCACTTTCTGGGTGATGAGATATGATGATCTGAGCA 379
Db 485 CTGGAGAAATCTGCTTCAATATCTTGACCTATTGGGTTCATGAGCGACATGAGACTGAGCG 544
Oy 380 TCAGTATGACAACTGCTTTCACCGTCCGCGCTGGGAAATGATGACCACTCTGCAATTATC 439
Db 545 TCAGTATGACAACTGCTTTCACCGTCCGCGCTGGGAAATGATGACCACTCTGCAATTATC 604
Oy 440 TCTACACCTGCTGCTGAGAGCTTTCAGACAAATCTCAACATCTCTTATCAGAAATGAGAA 499
Db 605 TCTATACCAAAATGCTGCTGAGAGCTTTCAGACAAATCTCTTATGATTAACATAGTAA 664
Oy 500 TTACCTGTGTGCTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
Db 665 CATCTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Oy 560 CAACCAATCCAAATCATCTTCAGATTGGGCGCT 596
Db 724 CCAAA-AAGCAAGATCATCTTAAATGGGCTCAT 759

RESULT 9
BE151388 274 bp mRNA linear EST 21-JUN-2000
LOCUS CM2-HT0285-081199-026-a09 HT0285 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE151388
VERSION BE151388.1 GI:8614109
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 274)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.D.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=62-CW2-HT0285-081
199-026-a09&ct3=1999-11-08&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 109.
Location/Qualifiers
1. 274
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0285"

/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site: 1: SmaI;
Site: 2: SmaI; A mini-library was made by cloning products
derived from ORFESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 82 a 71 c 71 g 50 t
ORIGIN
Query Match 16 2%; Score 184; DB 10; Length 274;
Best Local Similarity 96.8%; Pred. No. 3.5e-42;
Matches 209; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
Oy 164 TCCGAGAGCTGTGTGACATCAGAGACCTGGGGGATGCTGAGACTGCTGCGC 223
Db 272 TACGGAATCCGTTTCCGACATCAGAGAACCTGGGGCATTTGCTGGGACTGCTGCC 213
Oy 224 AG-TTGGGCTCATGCTTTTACAGCTTATCTCTGGCCATTAGCTTTTCTGAAAGCA 282
Db 212 AGTTTGGGCTCATGCTTTTACAGCTTATCTCTGGCCATTAGCTTTTCTGAAAGCA 153
Oy 283 GTCCAGCTATGCTGCTCTCATCATGAGGCTGCTGCC-CCGGGGGACACCATCTTAACAT 341
Db 152 GTCCAGCTATGCTGCTCTCATCATGAGGCTGCTGCC-CCGGGGGACACCATCTTAACAT 93
Oy 342 TTTCACTTCTGGGTTGATGAGATATGATGATCAG 377
Db 92 TTTCACTTCTGGGTTGATGAGATATGATGATCAG 57

RESULT 10
AQ013853/c 543 bp DNA linear GSS 14-APR-1999
LOCUS RPCI11-2407.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-2407,
DEFINITION AQ013853
VERSION AQ013853
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 543)
Adams,M.D., Rounley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
JOURNAL RPCI11-2407.TKBF
COMMENT Other_GSSes: RPCI11-2407.TKBF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hunguen/bac_end_search/bac_end_search.html
Class: BAC ends.
Location/Qualifiers
1. 543
/organism="Homo sapiens"
/db_xref="GDB:7509174"
/db_xref="taxon:9606"
/clone_lib="RPCI-11-2407"
/clone_lib="RPCI-11"
/sex="Male"

/cell_type="Lymphocytes"
/note="Vector: PBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC11 Human Male BAC Library"

BASE COUNT

168 a 118 c 97 g 160 t

Query Match

Best Local Similarity 16.1%; Score 182.6; DB 17; Length 543;
Matches 188; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 578 TTCGACAGTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 637
DB 493 TGTCTGACATTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 434
QY 638 TGTCTGACATTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 697
DB 433 TGTCTGACATTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 374
QY 698 TGTCTGACATTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 757
DB 373 TGTCTGACATTTGGGCGCGTTGTTGGTGGGCTCTCTCTGTTGGTGGCAGTTGGTG 314
QY 758 AAAGGTGACAGCAATT 774
DB 313 AAAGGTATGTTAACT 297

RESULT 11

BE030429 538 bp mRNA linear EST 09-JUL-2000
LOCUS BE030429 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.

DEFINITION BE030429
ACCESSION BE030429
VERSION BE030429.1 GI:8325438
KEYWORDS EST.

SOURCE

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 538)
AUTHORS Rahnenflug, S.C., Preking, B.A., Rohrer, G.A., Smith, T.P.L., Caeas, E.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Iaegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL

COMMENT

Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCACAGTACGACG
Plate: 58 row: A column: 1
Seq primer: ATTAGTACACATATAG.
Location/Qualifiers

FEATURES

source

1..538
/organism="Sus scrofa"
/db_xref="taxon:9623"
/clone_1ib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT

107 a 142 c 153 g 136 t

Query Match 14.5%; Score 164.6; DB 10; Length 538;

Best Local Similarity 69.3%; Pred. No. 1.8e-36;
Matches 224; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 125 TGGGCTCTCATGTTCTCTTTGGATGTTCCGTGAGATCCGGAAGCTGTGTCGACA 184
DB 183 TGGGCTCTCATGTTCTCTTTGGATGTTCCGTGAGATCCGGAAGCTGTGTCGACA 242
QY 185 TCAGAGACCCCTGGGGGACATGCTGTGGAGACGCTGTGACGTTGGGCTGATGCTTTA 244
DB 243 TAAAGGACCCCTGGGGGACATGCTGTGGAGACGCTGTGACGTTGGGCTGATGCTTTA 302
QY 245 CAGCTTATCTCTGCGCCATTAGCTTTCTGAAAGCCAGTCCAAAGTATGCTGTTCA 304
DB 303 CGGGCTCATCTATGATGAGCTTTTGAATCCCTGTCGACGCTGAGGATGATCA 362
QY 305 TCATGAGCTGCTGCCCGGGGACACATCTTAACATTTTCACTTCTGAGTATGAG 364
DB 363 TAAATGGATGCTGTCCAGAGAGGACCTTCTCAACATCTTGGCTTACTGGGTTGATGCG 422
QY 365 ATATGATCTGAGCATGATGATGACATCTGTCACCGTGGCGCCCTGGGAATGATG 424
DB 423 AATGATCTGAGCATGATGATGACATCTGTCACCGTGGCGCCCTGGGAATGATG 482
QY 425 CACTCTGATTTATCTTACAC 447
DB 483 CGCTGTGCTCTTATCTATAC 505

RESULT 12

AW107022 686 bp mRNA linear EST 20-OCT-1999
LOCUS AW107022
DEFINITION AW107022 un18f05.v1 Sugano mouse kidney m1a Mus musculus cDNA clone
IMAGE:2192673.5; similar to TR:P0172 P0172 ILEAL NA+-DEPENDENT
BILE ACID TRANSPORTER ; mRNA sequence.

ACCESSION AW107022
VERSION AW107022.1 GI:6077890
KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriongnath; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 686)
Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter,
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

JOURNAL

COMMENT

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1005125
Seq primer: custom primer used
High quality sequence stop: 491.

FEATURES

source

1..686
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2192673"
/clone_1ib="Sugano mouse kidney m1a"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGCTG); Site 2: DraIII (CACCATGTC); 1st strand cDNA
was primed with an oligo(dT) primer

OY	140	TCCTCTTTGGGAAGTTCCGGTGGAGATCCGGAACTGGAGTGGAGCAATACAGAAACCCCTGGG	199
Db	245	TTTCTATGGGGTGCAATGTGGAAATGCCACAGTTCTCTAGACATATTAAGAGCCATGGG	304
OY	200	GCATTGCTGTGGGACTGCTCTGCCAGTTTGGGGCTCATGCGCTTTACAGCTTATCTCTGG	259
Db	305	GTATCTTGTGGGCTTCCCTCTCTCAAGTTTGGAAATATGCTCTCACAGGCTTTATCTGT	364
OY	260	CCATTAGCTTTCTCTGGAAGCCAGTCCAAAGCTATGTCTGTTCATCATGGGCTGTGCGC	319
Db	365	CTGTGGCCCTGGCATTCTCTCTGTACAGGCTGTAGTGCTGAATATAGGGTGTGCGC	424
OY	320	CGGGGGGCAACATCTCTTACATTTTTCACCTTCTGGGTTGATGAGATATGATCTCAGCA	379
Db	425	CTGGGGAACCTGGCTTCCCAATATCTGGGCTTATTTGATATGATGGCGCATTTGGACCTCAGTG	484
OY	380	TCAGATATACAACTGTTCACACCGTGGCCGGCCCTGGGAATATAGGCACCTCTGACATTATC	439
Db	485	TTAGCATATACCACTTGTCTCCACACAGTGTTCGCCCTTGGAAATGATAGCCCTTTTGTGCTTTTTCG	544
OY	440	TCATACCTGAGCTCGAGATCTTTCAGCAGAA	470
Db	545	TTTACACCCCAATGTGGGTGAACCTTCGGAA	575

RESULT 14				
BI149148	BI149148	919 bp	mRNA	linear EST 05-JUL-2001
LOCUS				
DEFINITION	602912278F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5053578 5',			

ACCESSION	BI149148	GT:14609149
VERSION	BI149148.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 919)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MSC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
 Plate: L14M1145 row: K column: 19
 High quality sequence start: 9
 High quality sequence stop: 901.
 Location/Qualifiers
 1..919

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BASE COUNT      202 a      265 c      230 g      222 t
ORIGIN
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:5053578"
/clone_id="NCI CGAP L19"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP library."

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	Query Match	Score	DB 13	Length	919
	12.5%	142.2	DB 13	Length	919
	Best Local Similarity	56.1%	Pred. No.	6.9e-30	
	Matches 289	Conservative	0	Mismatches	223
				Indels	3
				Gaps	1
QY	118	GTGATGATGGGGCTGTCATGTTCTTTGGGATGTTCCCTGGAGATCCCGGAGCTGTG	177		

Db 232 GTTATCTTCTCTCATCATCTCTCTCGGTCGTCGACCATGAGTTTCAGCAAGATCAAG 291

Oy 178 TCGCACAATGAGAGACCTTGGGGCAATGCTGTGGAAGCTGCTTGGCCAGTTTGGGCTTCATG 237

Db 292 GCTCATCTTCTGGAAAGCCCAAAGGGGTGATCATCCGCATAGTGCCGAGTACGGTATCATG 351

Oy 238 CCTTTACAGCTTATCTCTGTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAAGCATATTGCT 297

Db 352 CCCCTCAGTCTTCTCTGTGGCAAGGCTTTTATCTGACACAGCATTTGAGGCTCTGGCC 411

Oy 298 GTTCTCATCATGGGCTGTGCCCCGGGGGGGACCAATCTCTACATTTTCACCTTCTGGGTT 357

Db 412 ATCTCATCTGGGGTGTCTCTCTGTGGGGGAACCTGTCTAACCTCTTCAACCTCTGGCATG 471

Oy 358 GATGAGATATGAGATCTCAGATCAATGACAACTGTGTCACCGTGGCCGCCCTGGGA 417

Db 472 AAGGGGGAATGAACCTCAGCATGTGTGATGACACACTGCTCAAGCTTCACTGCTTGGGC 531

Oy 418 AATATGCCACTCTGCACTTTATCTCTACACCT---GCTCTGGAATCTTCAAGCAAAATCTC 474

Db 532 ATGATCCCTCTCCTCTTATACATCTACAGCAAAAGAAATCTTACGAGGAGATCTTAAAGAC 591

Oy 475 ACCATTCCTTATCAGAACATAGAAATTAACCTGTGTGCTCGACCAATTCCTGTGGGCTTT 534

Db 592 AAGGTGCCCTCAAAAGGCAATTATGTTATCACTGTGCAAGTTCATTTCTTGTGGCCATA 651

Oy 535 GGTGTCTATGTGAATTACAGATGAGCCAAACATCCAAATCAATTTCTCAAGATTGGGCCC 594

Db 652 GGGATCTTCTCTAAGTCCAAAGGCCACACATATGACCTTACGTCTCAAGGAGGCGATG 711

Oy 595 GTTGTGTGGGGTCTCTCTCTGTGGTGTCCAGT 629

Db 712 ATCATACCTTCTCCCTCTCTGTGGCTGTCAAGT 746

RESULT 15
 Locus BF234728 876 bp mRNA linear EST 14-NOV-2000
 Definition 6020285551 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4163893 5',
 Accession BF234728
 Version BF234728
 Keywords BF234728.1 GI:11146527
 Source Est.
 Organism house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 876)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: CGAPds-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LHAM9448 row: m column: 14
 High quality sequence stop: 664.
 Location/Qualifiers
 1..876

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/cclone="IMAGE:4163893"
/cclone_id="NCI_CGAP_l1.9"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: liver; Vector: PCMV-SpOR6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt

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Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library.
BASE COUNT 190 a 265 c 222 g 198 t 1 others
ORIGIN

Query Match 12.5%; Score 141.2; DB 12; Length 876;
Best Local Similarity 55.9%; Pred. No. 1,3e-29;
Matches 288; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

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QY 118 GTGATGATGGGCTGCTCAATGTTCTTTGGAGATGTTCCGTGGAGATCCGGAAGCTGTG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 183 GTTATGTTGCTGCTCAATGCTCTGCTTGGCTGACCACTGAGATTCAAGATCAAG 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 TCGACATAGAGAGACCTGGGCAATTGCTGTGGGACTGCTGACGATTGGGCTCATG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 243 GCTCATCTTCTGGAAGCCCAAGGGGTGATCATGCGCATAGTGGCCAGTACGGTATCATG 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 CCTTTACAGCTTATCTCCCTGGGCAATTAGCTTTCTGTGAAGCCAGTCCAGCTATTGCT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 303 CCCCTGAGTCTTCTTCTGGGCAAGTCTTTCATCTGACGACATGAGGCTGTGGCC 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 GTTCTCATGAGGCTGTGCTGCCGGGGGGCACCATCTCTTAACATTTTCACTTGGGTT 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 363 ATCCTCATCTGCGGCTGCTCTCTGGGGGGAACCTGTCTAACCTCTTCAOCTGGGCATG 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 GATGAGATATGATCTCAGCATCAGTATGACAACTGTTCCACCGTGGCCGCTGGGA 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 423 AAGGGGGAACATGAACCTCAGCATGTGATGACCACTGCTCCAGCTTCACTGGCTTGGGC 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 ATGATGCCACTCTGCATTTATCTCTACACT---GGTCTGAGTCTTCAAGCAGATCTC 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 483 ATGATGCCCTCTCTTTATACATCTACAGCAAGAAGATCTACGAGAGATCTTAAGAC 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 ACCATTCCTTATCAGAACAATAGGAATTACCTGTGTGCTGACCATTCCTGTGGCCTT 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 543 AAGGTGCCCTACAAAGGCAATATGTTATCACTGTCATGTGTTCTCATTCCTTGGGCATA 602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 GGTGCTTATGTGATTAACAGATGGCCAAACAATCCAAAATCATTTCTCAAGATTGGGCC 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 603 GGGATCTTCTGGAAGTCCAAAGGGGCACTATGTACCTTACGTCCTCAAGGCGAGCATG 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 GTTGTGTGGGGTCTCTCTTCTGTGGTGGTGGAGT 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 663 ATCATCATTTCTCCCTCTCTGTGGCTGTACAGT 697
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Search completed: June 9, 2003, 07:06:01
Job time : 1872 secs